



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 6, 2023 – 01:11 am GMT

PDB ID : 2JBU
Title : Crystal structure of human insulin degrading enzyme complexed with co-purified peptides.
Authors : Im, H.; Shen, Y.; Tang, W.J.
Deposited on : 2006-12-11
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

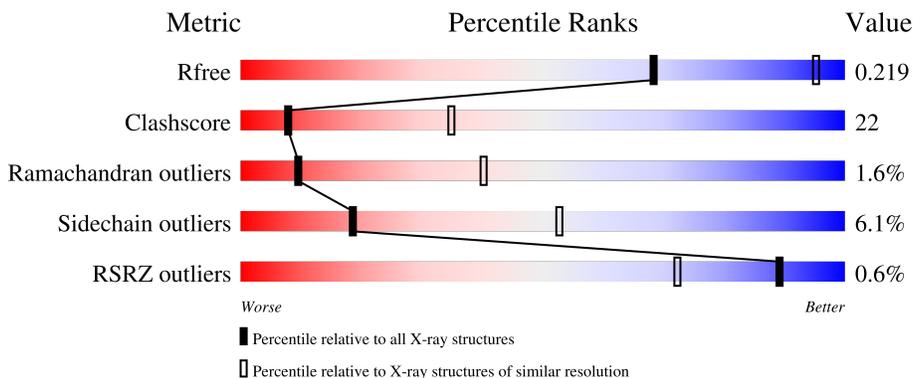
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	990	 58% 35% 5% .
1	B	990	 55% 37% . .
2	C	12	 75% 8% 17%
2	D	12	 67% 17% 17%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15897 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called INSULIN-DEGRADING ENZYME.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	963	7859	5058	1318	1448	35	0	0	1
1	B	961	7846	5049	1316	1446	35	0	0	1

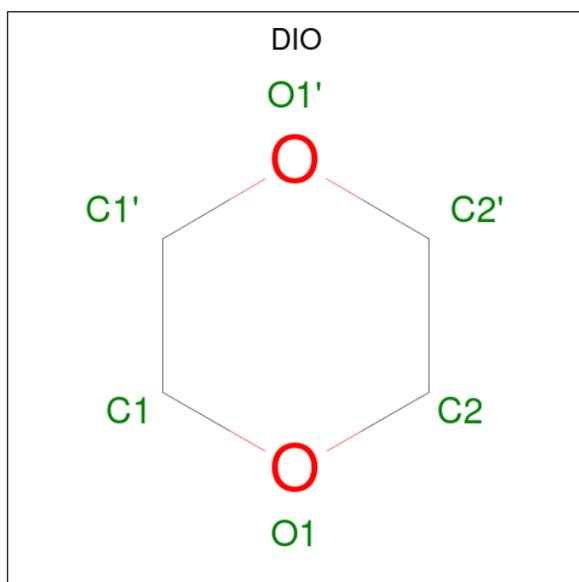
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	111	GLN	GLU	engineered mutation	UNP Q5T5N2
B	111	GLN	GLU	engineered mutation	UNP Q5T5N2

- Molecule 2 is a protein called CO-PURIFIED PEPTIDE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	10	50	30	10	10	0	0	0
2	D	10	50	30	10	10	0	0	0

- Molecule 3 is 1,4-DIETHYLENE DIOXIDE (three-letter code: DIO) (formula: C₄H₈O₂).

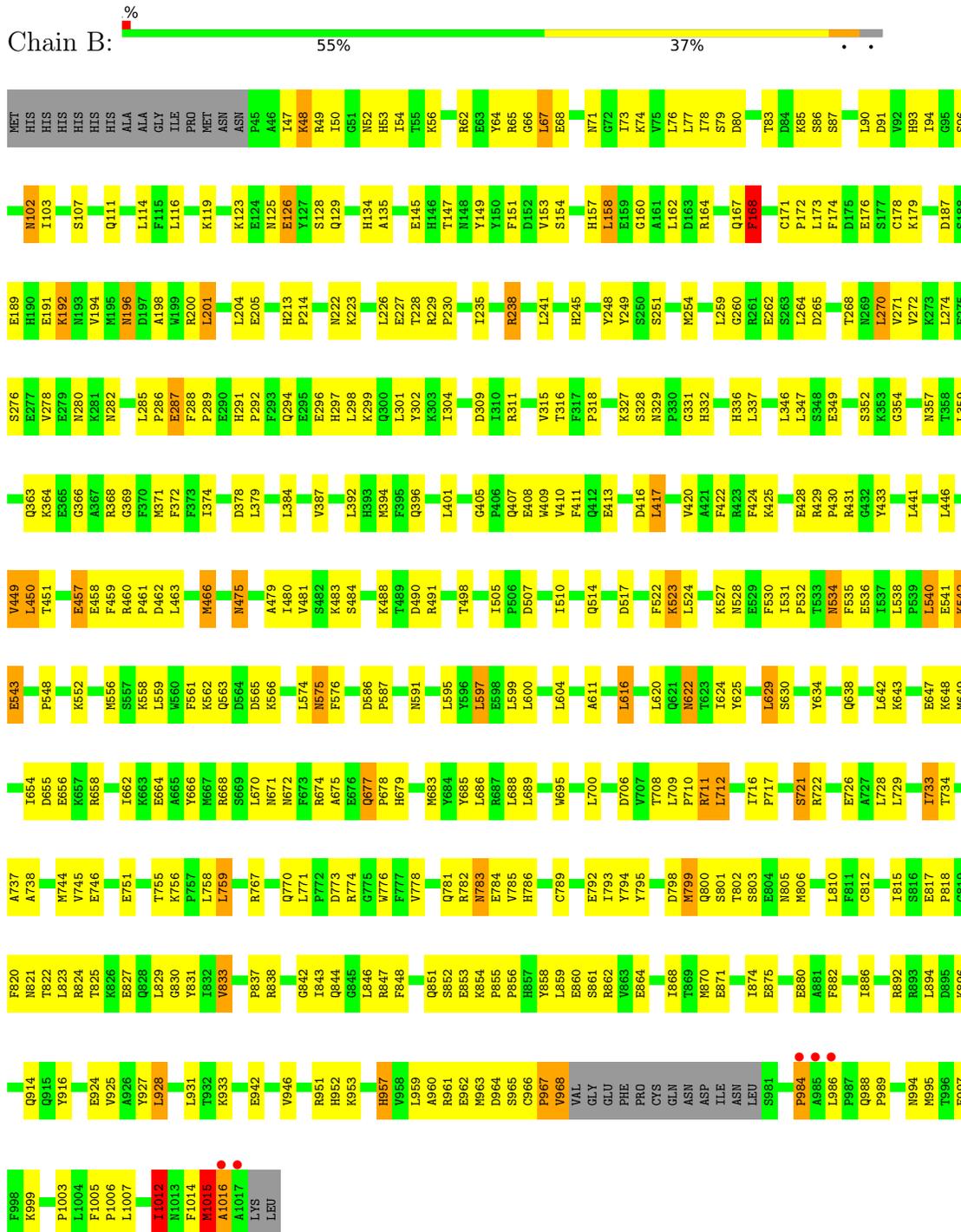


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf		
3	A	1	Total	C	O	0	0
			6	4	2		
3	B	1	Total	C	O	0	0
			6	4	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
4	A	44	Total	O	0	0
			44	44		
4	B	35	Total	O	0	0
			35	35		
4	D	1	Total	O	0	0
			1	1		

- Molecule 1: INSULIN-DEGRADING ENZYME



- Molecule 2: CO-PURIFIED PEPTIDE



- Molecule 2: CO-PURIFIED PEPTIDE



4 Data and refinement statistics i

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	263.28Å 263.28Å 90.73Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.86 – 3.00 49.75 – 2.99	Depositor EDS
% Data completeness (in resolution range)	98.1 (29.86-3.00) 98.0 (49.75-2.99)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.42 (at 3.01Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.186 , 0.240 0.173 , 0.219	Depositor DCC
R_{free} test set	3670 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	52.4	Xtrriage
Anisotropy	0.143	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 59.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.027 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	15897	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.97% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: DIO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.51	0/8056	0.72	1/10896 (0.0%)
1	B	0.47	0/8043	0.69	1/10877 (0.0%)
2	C	0.93	0/48	0.72	0/64
2	D	0.75	0/48	0.72	0/64
All	All	0.49	0/16195	0.71	2/21901 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	168	PHE	N-CA-C	-7.20	91.55	111.00
1	A	429	ARG	N-CA-C	-5.38	96.47	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7859	0	7788	310	0
1	B	7846	0	7776	372	0
2	C	50	0	51	3	0
2	D	50	0	51	3	0
3	A	6	0	8	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	6	0	8	2	0
4	A	44	0	0	2	0
4	B	35	0	0	4	0
4	D	1	0	0	0	0
All	All	15897	0	15682	679	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 22.

The worst 5 of 679 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:810:LEU:HD23	1:B:928:LEU:HD21	1.30	1.12
1:A:538:LEU:HD23	1:A:734:THR:HG23	1.38	1.06
1:B:599:LEU:HD23	1:B:662:ILE:HD12	1.39	1.01
1:A:309:ASP:H	1:A:672:ASN:HD21	1.11	0.98
1:B:309:ASP:H	1:B:672:ASN:HD21	1.02	0.98

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	959/990 (97%)	885 (92%)	61 (6%)	13 (1%)	11	43
1	B	957/990 (97%)	861 (90%)	79 (8%)	17 (2%)	8	37
2	C	6/12 (50%)	5 (83%)	1 (17%)	0	100	100
2	D	6/12 (50%)	6 (100%)	0	0	100	100
All	All	1928/2004 (96%)	1757 (91%)	141 (7%)	30 (2%)	9	40

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	981	SER
1	B	48	LYS
1	B	52	ASN
1	B	984	PRO
1	B	1012	ILE

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	859/883 (97%)	808 (94%)	51 (6%)	19 54
1	B	858/883 (97%)	804 (94%)	54 (6%)	18 51
All	All	1717/1766 (97%)	1612 (94%)	105 (6%)	18 53

5 of 105 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	168	PHE
1	B	466	MET
1	B	964	ASP
1	B	196	ASN
1	B	287	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	805	ASN
1	B	887	GLN
1	A	828	GLN
1	A	805	ASN
1	B	917	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	DIO	A	1101	-	6,6,6	0.74	0	6,6,6	0.26	0
3	DIO	B	1101	-	6,6,6	0.76	0	6,6,6	0.25	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DIO	A	1101	-	-	-	0/1/1/1
3	DIO	B	1101	-	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1101	DIO	3	0
3	B	1101	DIO	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	D	1
2	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	3:ALA	C	6:ALA	N	12.43
1	C	3:ALA	C	6:ALA	N	12.25

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	963/990 (97%)	-0.58	6 (0%) 89 72	15, 34, 60, 96	0
1	B	961/990 (97%)	-0.49	5 (0%) 91 75	19, 44, 71, 98	0
2	C	10/12 (83%)	0.11	0 100 100	30, 60, 73, 75	0
2	D	10/12 (83%)	-0.13	0 100 100	29, 61, 76, 80	0
All	All	1944/2004 (97%)	-0.53	11 (0%) 89 72	15, 39, 68, 98	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	985	ALA	3.3
1	B	984	PRO	3.1
1	A	1015	MET	3.1
1	A	1013	ASN	3.1
1	A	984	PRO	2.9

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	DIO	A	1101	6/6	0.97	0.23	45,55,60,61	0
3	DIO	B	1101	6/6	0.98	0.24	26,34,43,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.